REMARKS

In response to the Notice to Comply with Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures dated November 23, 2004 (copy enclosed), Applicants have amended the specification to include the required sequence identifiers and substitute Sequence Listing. A computer readable form (CRF) copy of the enclosed substitute Sequence Listing and a Statement As Required Under 37 C.F.R. § 1.825(a) and (b) And Statement As Required Under 37 C.F.R. § 1.821(g) are also submitted herewith. No new matter is introduced by this amendment.

Should the Examiner have any questions or comments regarding this matter, a telephone call to the undersigned Applicants' representative is earnestly solicited.

Please date stamp and return the enclosed postcard evidencing receipt of these materials.

Respectfully submitted,

Michael R. Hayes (51,898)
Michael R. Krawzenek for:
Mark B. Wilson
Reg. No. 37,259
Agent for Applicants

FULBRIGHT & JAWORSKI L.L.P.
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Austin, Texas 78701
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512.536.4598 (fax)

Date: December 23, 2004

APPENDIX A

SEQUENCE LISTING

<110> SARCABAL, PATRICIA
CROUX, CHRISTIAN
SOUCAILLE, PHILIPPE

<120> METHOD FOR PREPARING 1,3-PROPANEDIOL BY A RECOMBINANT MICRO-ORGANISM IN THE ABSENCE OF COENZYME B12 OR ONE OF ITS PRECURSORS

<130> CHEP:004US

<140> 10/043,639
<141> 2002-01-09

<150> PCT/FR00/01981
<151> 2000-07-07

<150> FR 99/08939
<151> 1999-07-09

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<170> PatentIn Ver. 2.1

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Tyr His Asn Tyr Gly Glu Asn Lys Tyr Gln Ala Ile Gly Arg Glu Tyr
            260                 265                 270

Ser Leu Lys Glu Leu Lys Ser Pro Ser Lys Asp Lys Met Glu Arg Leu
        275                 280                 285

Lys Ala Leu Val Glu Ile Met Gly Ile Pro Cys Thr Ile Gly Ala Glu
    290                 295                 300
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<210> 8
<211> 385
<212> PRT
<213> Clostridium butyricum

<400> 8

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Met Arg Met Tyr Asp Tyr Leu Val Pro Ser Val Asn Phe Met Gly Ala
  1               5                  10                  15

Asn Ser Val Ser Val Val Gly Glu Arg Cys Lys Ile Leu Gly Gly Lys
             20                  25                  30

Lys Ala Leu Ile Val Thr Asp Lys Phe Leu Lys Asp Met Glu Gly Gly
         35                  40                  45

Ala Val Glu Leu Thr Val Lys Tyr Leu Lys Glu Ala Gly Leu Asp Val
     50                  55                  60

Val Tyr Tyr Asp Gly Val Glu Pro Asn Pro Lys Asp Val Asn Val Ile
 65                  70                  75                  80

Glu Gly Leu Lys Ile Phe Lys Glu Glu Asn Cys Asp Met Ile Val Thr
                 85                  90                  95

Val Gly Gly Gly Ser Ser His Asp Cys Gly Lys Gly Ile Gly Ile Ala
            100                 105                 110

Ala Thr His Glu Gly Asp Leu Tyr Asp Tyr Ala Gly Ile Glu Thr Leu
        115                 120                 125

Val Asn Pro Leu Pro Pro Ile Val Ala Val Asn Thr Thr Ala Gly Thr
    130                 135                 140

Ala Ser Glu Leu Thr Arg His Cys Val Leu Thr Asn Thr Lys Lys Lys
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145 150 155 160

Ile Lys Phe Val Ile Val Ser Trp Arg Asn Leu Pro Leu Val Ser Ile
165 170 175

Asn Asp Pro Met Leu Met Val Lys Lys Pro Ala Gly Leu Thr Ala Ala
180 185 190

Thr Gly Met Asp Ala Leu Thr His Ala Ile Glu Ala Tyr Val Ser Lys
195 200 205

Asp Ala Asn Pro Val Thr Asp Ala Ser Ala Ile Gln Ala Ile Lys Leu
210 215 220

Ile Ser Gln Asn Leu Arg Gln Ala Val Ala Leu Gly Glu Asn Leu Glu
225 230 235 240

Ala Arg Glu Asn Met Ala Tyr Ala Ser Leu Leu Ala Gly Met Ala Phe
245 250 255

Asn Asn Ala Asn Leu Gly Tyr Val His Ala Met Ala His Gln Leu Gly
260 265 270

Gly Leu Tyr Asp Met Ala His Gly Val Ala Asn Ala Met Leu Leu Pro
275 280 285

His Val Glu Arg Tyr Asn Met Leu Ser Asn Pro Lys Lys Phe Ala Asp
290 295 300

Ile Ala Glu Phe Met Gly Glu Asn Ile Ser Gly Leu Ser Val Met Glu
305 310 315 320

Ala Ala Glu Lys Ala Ile Asn Ala Met Phe Arg Leu Ser Glu Asp Val
325 330 335

Gly Ile Pro Lys Ser Leu Lys Glu Met Gly Val Lys Gln Glu Asp Phe
340 345 350

Glu His Met Ala Glu Leu Ala Leu Leu Asp Gly Asn Ala Phe Ser Asn
355 360 365

Pro Arg Lys Gly Asn Ala Lys Asp Ile Ile Asn Ile Phe Lys Ala Ala
370 375 380

Tyr
385

<210> 9
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 9
cgcggatccg tgattggagg agtaaaaatg ataag 35

<210> 10
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
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Primer

<400> 10
tcccccgggg gaatccttta aatagtatta attaataagc 40

<210> 11
<211> 34
<212> DNA
<213> Artificial Sequence

<400> 11
gttacccggg gctcctgcag ctcgactttt taac 34

<210> 12
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 12
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<210> 13
<211> 31
<212> DNA
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<220>
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Primer

<400> 13
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<210> 14
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<212> DNA
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<223> Description of Artificial Sequence: Synthetic
Primer

<400> 14
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